B2

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the proteins of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to possess the desired ability to degrade or catabolize fumonisin. Obviously, the mutations that will be made in the DNA encoding the variant must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure. See, EP Patent Publication No. 75,444.

Please revise the first full paragraph beginning on line 11, page 9, to read as follows:

B3

The carboxylesterase and amine oxidase have been previously described in U.S. Patent No. 5,716,820, U.S. Patent No. 6,025,188, and U.S. Patent No. 6,229,071. Such disclosures are herein incorporated by reference. Thus, the sequences of the invention can be used in combination with those previously disclosed or disclosed in U.S. Patent No. 6,211,435 and U.S. Patent No. 6,211,434, both entitled "Amino Polyolamine Oxidase Polynucleotides and Related Polypeptides and Methods of Use", herein incorporated by reference. These exemplary amino polyolamine oxidase nucleotide sequences are set forth in SEQ ID NOs: 16, 18, 20, 22, 24, 26, 28, 30, and 32. SEQ ID NO:16 is the same as SEQ ID NO:5 from U.S. Pat. No. 6,211,435; SEQ ID NO:18 is the same as SEQ ID NO:10 from U.S. Pat. No. 6,211,435; and SEQ ID NO:20 is the same as SEQ ID NO:22 from U.S. Pat. No. 6,211,435. The nucleotide sequences set forth in SEQ ID NOs: 16, 18, and 20 encode polypeptides having the amino acid sequences set forth in SEQ ID NOs: 17, 19, and 21, respectively (which are the same as SEQ ID NOs: 6, 11, and 23 from U.S. Pat. No. 6,211,435, respectively). Amino polyolamine oxidase nucleotide sequences of U.S. Pat. No. 6,211,434, with introns removed, are set forth in SEQ ID NOs:22 (SEQ ID NO:35 from U.S. Pat. No. 6,211,434), 24 (SEQ ID NO:37 from U.S. Pat. No. 6,211,434), 26 (SEQ ID NO:39 from U.S. Pat. No. 6, 211,434), 28 (SEQ ID NO:41 from U.S. Pat. No. 6,211,434), 30 (SEQ ID NO:43 from U.S. Pat. No. 6,211,434), and 32 (SEQ ID NO:45 from U.S. Pat. No. 6,211,434). The nucleotide sequences set forth in SEQ ID NOs: 22, 24, 26, 28, 30, and 32 encode polypeptides having the amino acid sequences set forth in SEQ ID NOs: 23, 25,

27, 29, 31, and 33, respectively (which are the same as SEQ ID NOs: 36, 38, 40, 42, 44, and 46 from U.S. Pat. No. 6,211,434, respectively). The enzymes and nucleotide sequences of the present invention provide a means for continued catabolism of the fumonisin-degradation products obtained after degradation with at least the carboxylesterase and amine oxidase.

Please revise the first full paragraph beginning on line 3, page 11, to read as follows:

By "fumonisin esterase" is meant any enzyme capable of hydrolysis of the ester linkage in fumonisin. Two examples of such enzymes are ESP1 and BEST1 found in U.S. Patent No. 5,716,820, U.S. Patent No. 6,025,188, and U.S. Patent No. 6,229,071. The ESP1 nucleotide sequence is set forth in SEQ ID NO:12 and is the same as SEQ ID NO:15 from U.S. Patent No. 6,025,188. This nucleotide sequence encodes a polypeptide having the amino acid sequence set forth in SEQ ID NO:13 (which is the same as SEQ ID NO:10 from U.S. Pat. No. 6,025,188). The BEST1 nucleotide sequence is set forth in SEQ ID NO:14 and is the same as SEQ ID NO:11 from U.S. Pat. No. 6,025,188. This nucleotide sequence encodes a polypeptide having the amino acid sequence set forth in SEQ ID NO: 15 (which is the same as SEQ ID NO:12 from U.S. Pat. No. 6,025,188).

Please revise the first full paragraph beginning on line 13, page 33, to read as follows:

Exophiala isolates from maize were isolated as described in U.S. Patent No. 5,716,820, U.S. Patent No. 6,025,188, and U.S. Patent No. 6,229,071, herein incorporated by reference.

Please revise the first full paragraph beginning on line 15, page 34, to read as follows:

Agar cultures grown as above were used to inoculate YPD broth cultures (500 ml) in conical flasks at a final concentration of 10^5 conidia per ml culture. Cultures were incubated 5 days at 28°C without agitation and mycelia harvested by filtration through 0.45 micron filters under vacuum. The filtrate was discarded, and the mycelial mat was washed and resuspended in sterile carbon-free, mineral salts medium (1 g/liter NH_3NO_4; 1 g/liter NaH_2PO_4; 0.5 g/liter $MgCl_2$; 0.1 g/liter NaCl; 0.13 g/liter $CaCl_2$; 0.02 g/liter $FeSO_4 \cdot 7H_20$, pH 4.5) containing 0.5

mg/ml alkaline hydrolyzed crude FB1. After 3-5 days at 28°C in the dark with no agitation the cultures were filtered through low protein binding 0.45 micron filters to recover the culture filtrate. Phenylmethyl sulfonyl fluoride (PMSF) was added to a concentration of 2.5 mM and the culture filtrate was concentrated using an Amicon™ YM10 membrane in a stirred cell at room temperature and resuspended in 50 mM sodium acetate, pH 5.2 containing 10 mM $CaCl_2$. The crude culture filtrate (approx. 200-fold concentrated) was stored at -20°C.

B4 cont'd

Please revise the first full paragraph beginning on line 26, page 37, to read as follows:

B1

The polynucleotides were identified using a proprietary transcript imaging method that compares transcript patterns in two samples and allows cloning of differentially expressed fragments. This technology was developed by CuraGen® (New Haven, Connecticut) (see PCT Patent Application No. WO 97/15690, published May 1, 1997 and claiming priority from U.S. Application No. 08/663,823, which issued as U.S. Patent No. 5,972,693, all of which are hereby incorporated by reference). Fluorescently-tagged, PCR amplified cDNA fragments representing expressed transcripts can be visualized as bands or peaks on a gel tracing, and the cDNA from differentially expressed (induced or suppressed) bands can be recovered from a duplicate gel, cloned, and sequenced. Known cDNAs can be identified without the need for cloning, by matching the predicted size and partially known sequence of specific bands on the tracing.

In The Claims:

Please amend the claims as follows:

B4 subst

1. (Amended) A method of reducing pathogenicity of a fungus that produces fumonisin, comprising:

a) stably integrating into the genome of a plant cell a primary nucleotide sequence operably linked to a first promoter active in said plant cell, said primary nucleotide sequence comprising at least one sequence selected from the group consisting of a